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GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLALRVARMPGLERSVRERFLPVH

Fig. 1

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CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC  
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CTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG  
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT  
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC  
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA  
GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT  
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GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG  
CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 3

SEQ ID No: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 SEQ ID No: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 SEQ ID No: 6 1  
 SEQ ID No: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG  
 G  
 SEQ ID No: 4 178 CA-TTCTGGAACCTACCTGGAGCGC  
 SEQ ID No: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG  
 SEQ ID No: 6 2 CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG  
 SEQ ID No: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG  
 SEQ ID No: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT  
 SEQ ID No: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT  
 SEQ ID No: 7 1 GAGGGGCCCCCAGGAGTGCTGCGCCACCCACAACCGTGCCCT  
 SEQ ID No: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT  
 SEQ ID No: 5 151 GCNGCTGCAGACCGGNTTCTTCGCGACGCTGNTTCTGCTTGAGCAC  
 SEQ ID No: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGACGCTGGTTTCTGCTTGAGCAC  
 SEQ ID No: 7 32 TGGCAGGGGTCAAGTTGCTGGTCCAGCCTTGACCCCTGAGCTAGGACAC  
 SEQ ID No: 3 151 GCCGCTGCCGCACCGGCTTCTTCGCGACGCTGGTTTCTGCTTGAGCAC  
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 SEQ ID No: 7 82 CAGTTCCCCTGACCCCTGTTCTTCCCCTCCTGGCTGCAGGACCCCCAGCCA  
 SEQ ID No: 8 1 GCATCGTGTCCACCTGGTGC CGCGTGATTGCCCGGACCCCCAGCCA  
 SEQ ID No: 10 1 CTTGTCCACCTGGTGC CGCGTGATTNCCC -GGCACCCCCAGCCA  
 SEQ ID No: 3 201 GCATCGTGTCCACCTGGTGC CGCGTGATTGCCCGGACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA-TGCAAGCCGTG  
 SEQ ID NO: 7 132 GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 8 51 GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 10 47 GAACACGCAGTGCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 9 1 AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT  
 SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC  
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT  
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 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGAACTGCACGGCCCTGGGCCT  
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Fig. 4 (cont.)

UNA 30942  
H1NFR2

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DNA 30942  
H1NFR2

CRD1 CRD2  
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DNA 30942  
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DNA 30942  
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DNA 30942  
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H1NFR2

443 S T E E K P L P L G V P D A G M K P S

Fig. 5

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31  
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P . . . . . 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62  
 OPG 26 . . P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93  
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124  
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155  
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4

DcR3 156 G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S 186  
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217  
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T . P R 247  
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L . L V R L L 277  
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300  
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

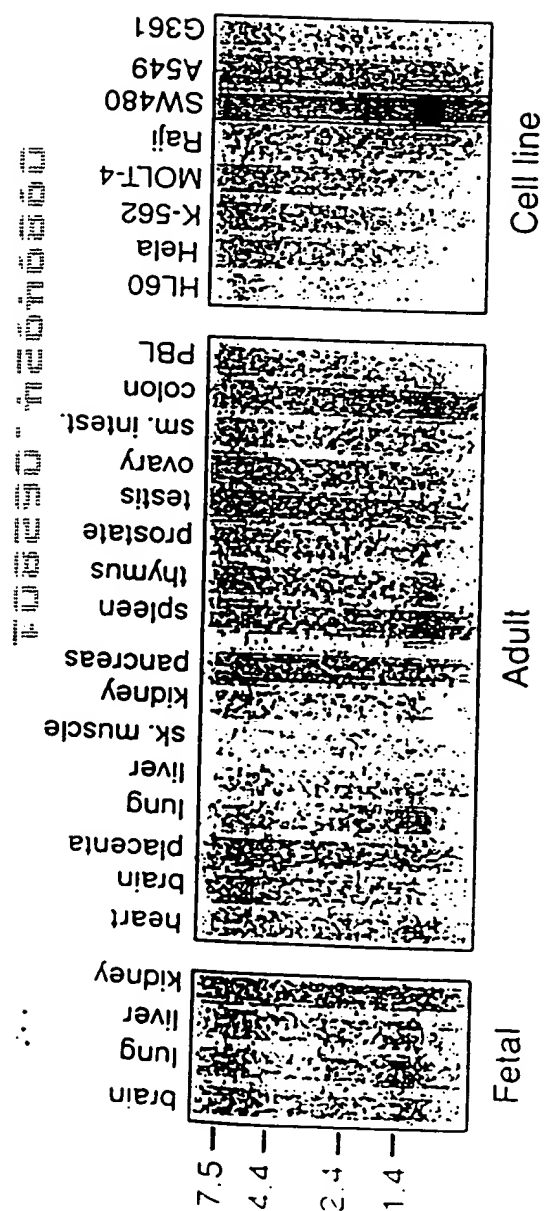


Fig. 7



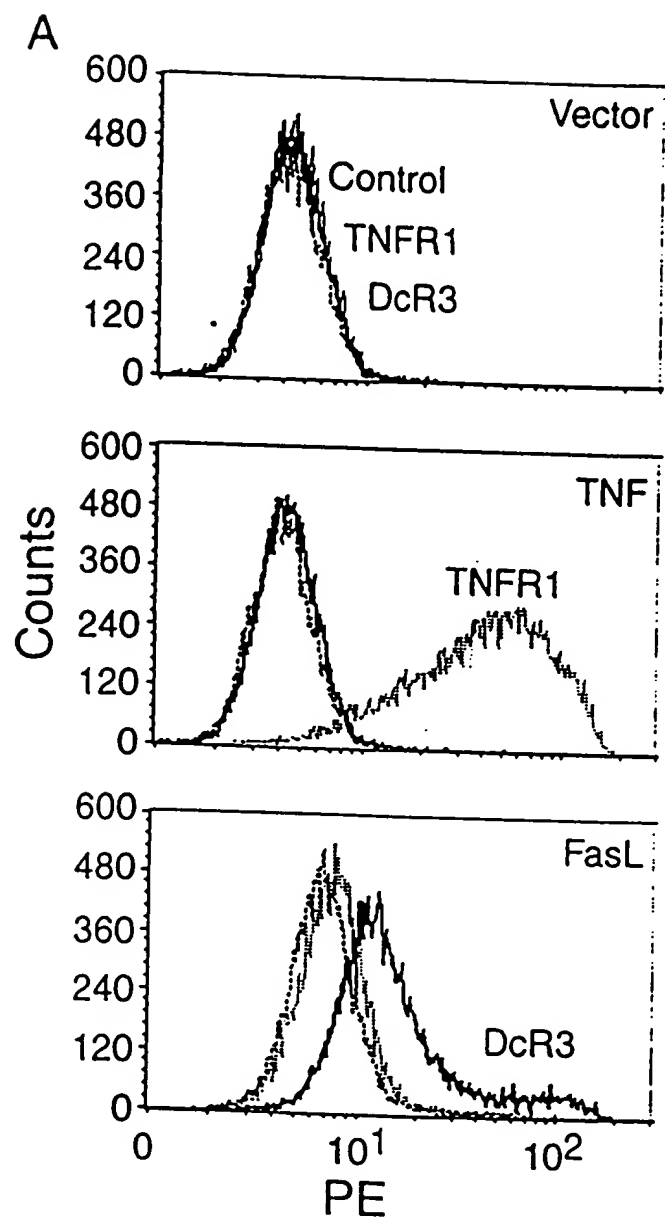
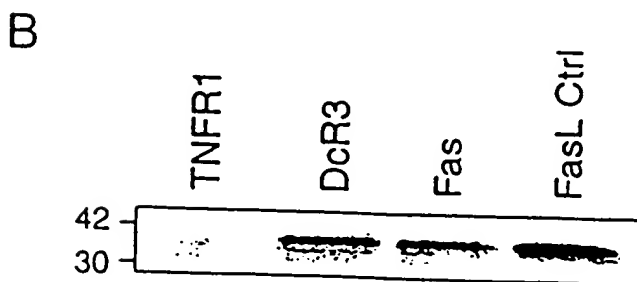


Fig. 8



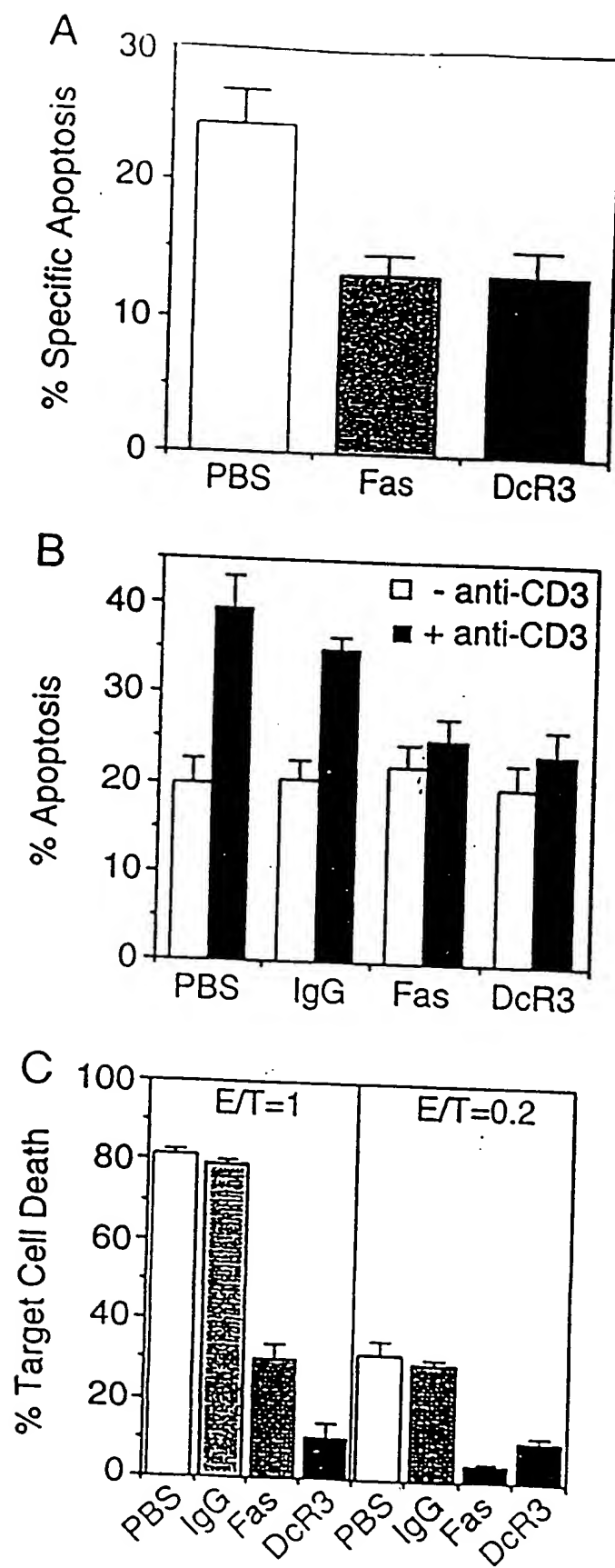


Fig. 9

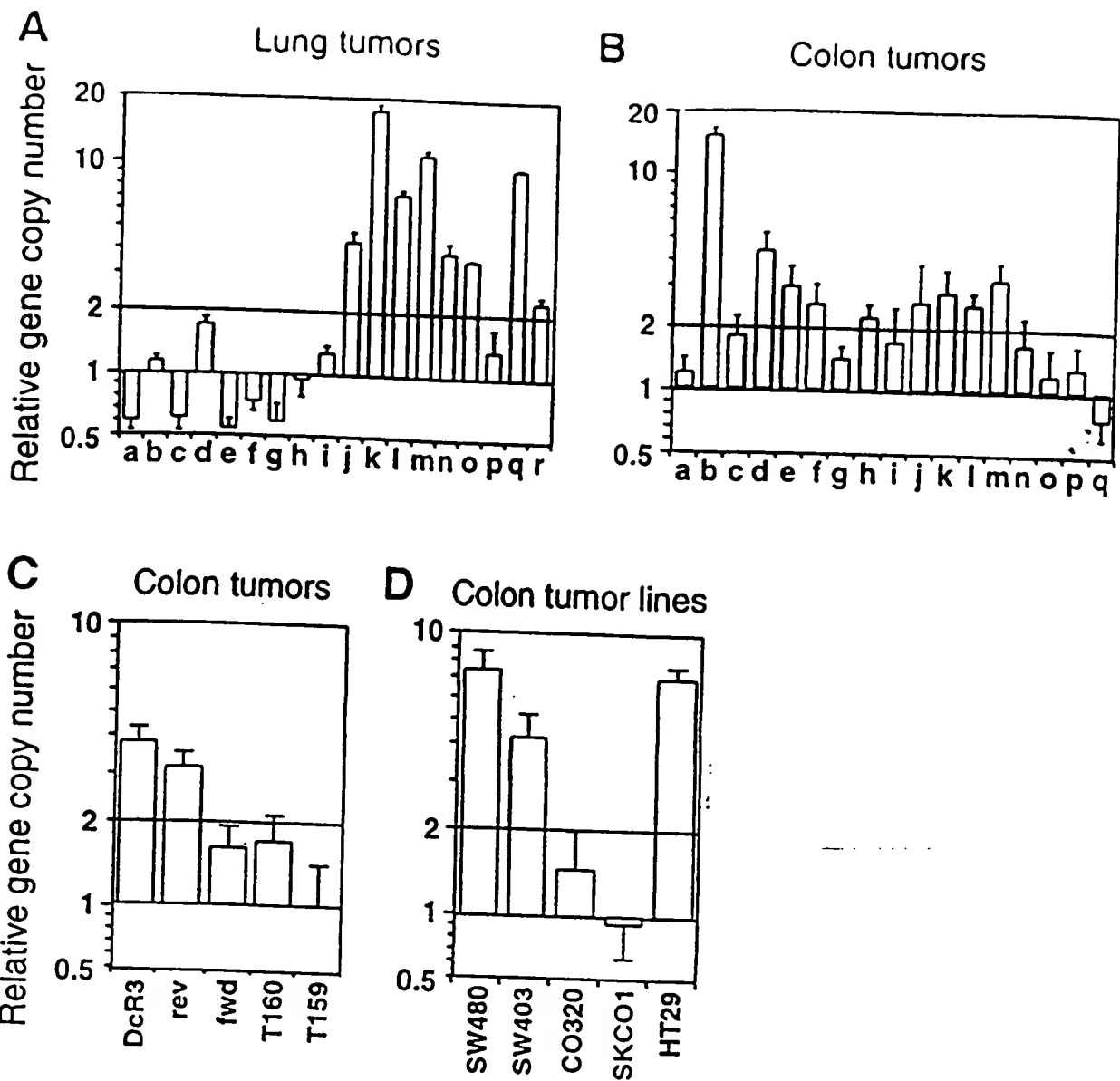


Fig. 10

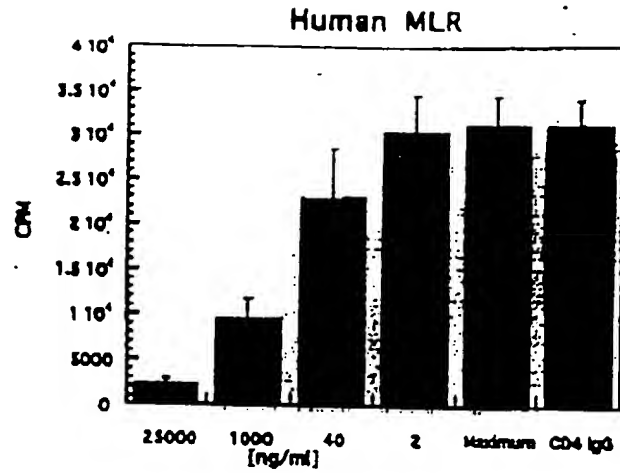


Fig. 11A

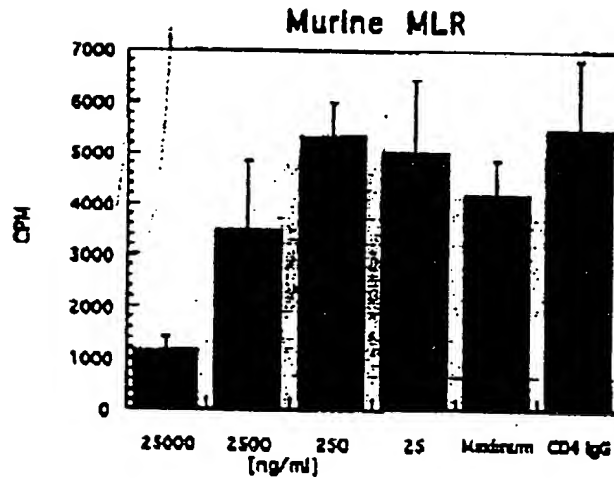


Fig. 11B

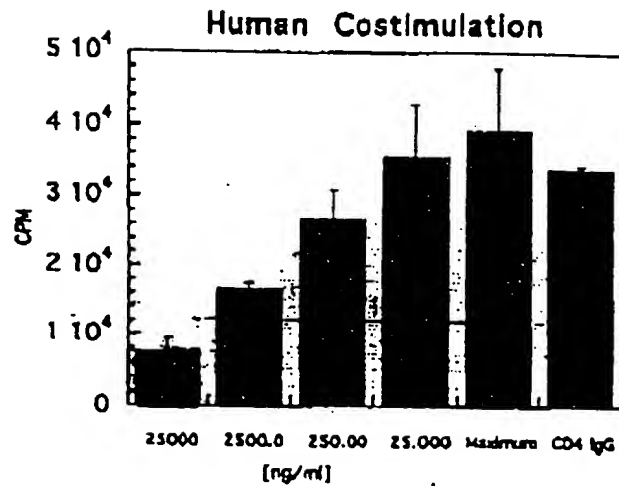


Fig. 11C



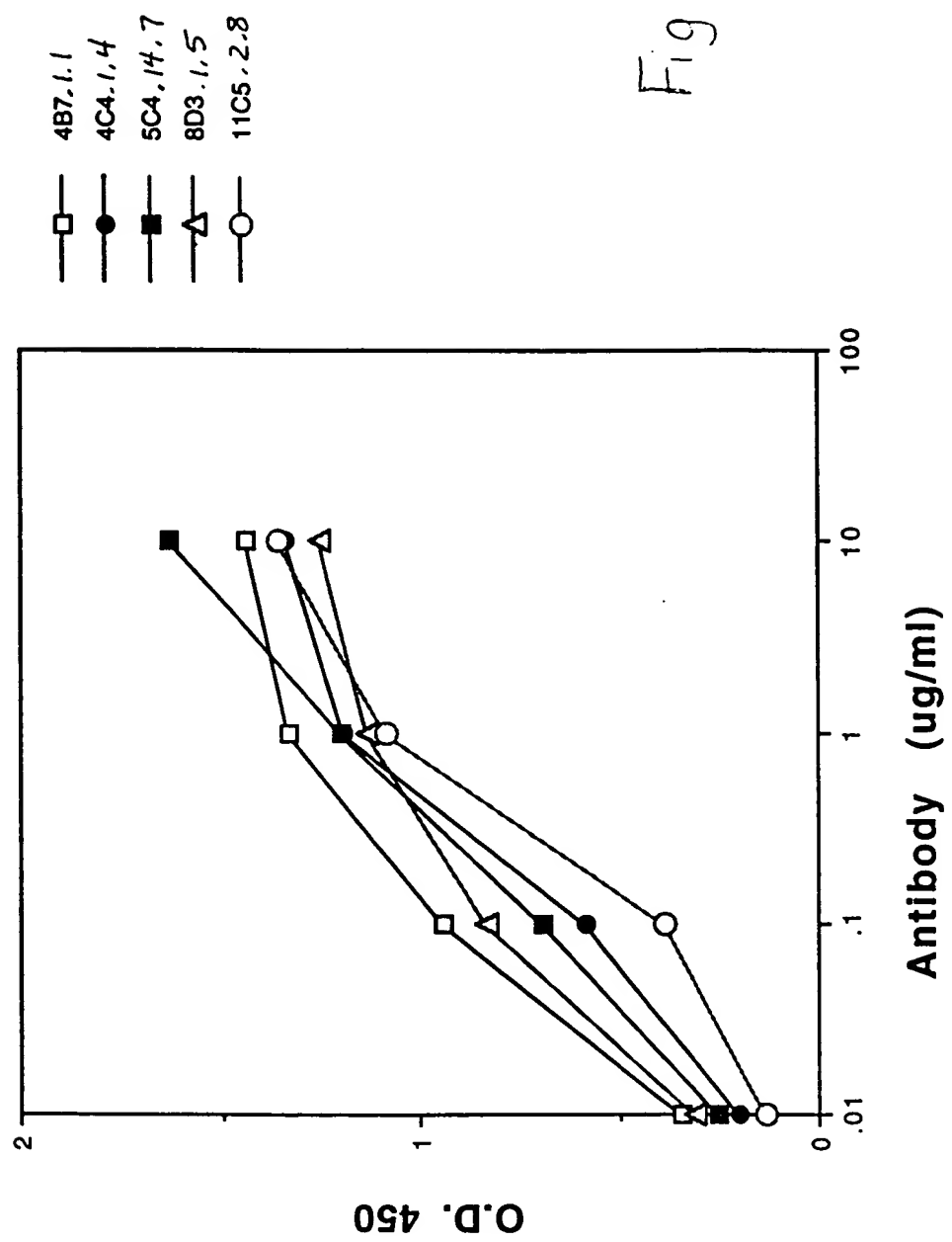


Fig. 13

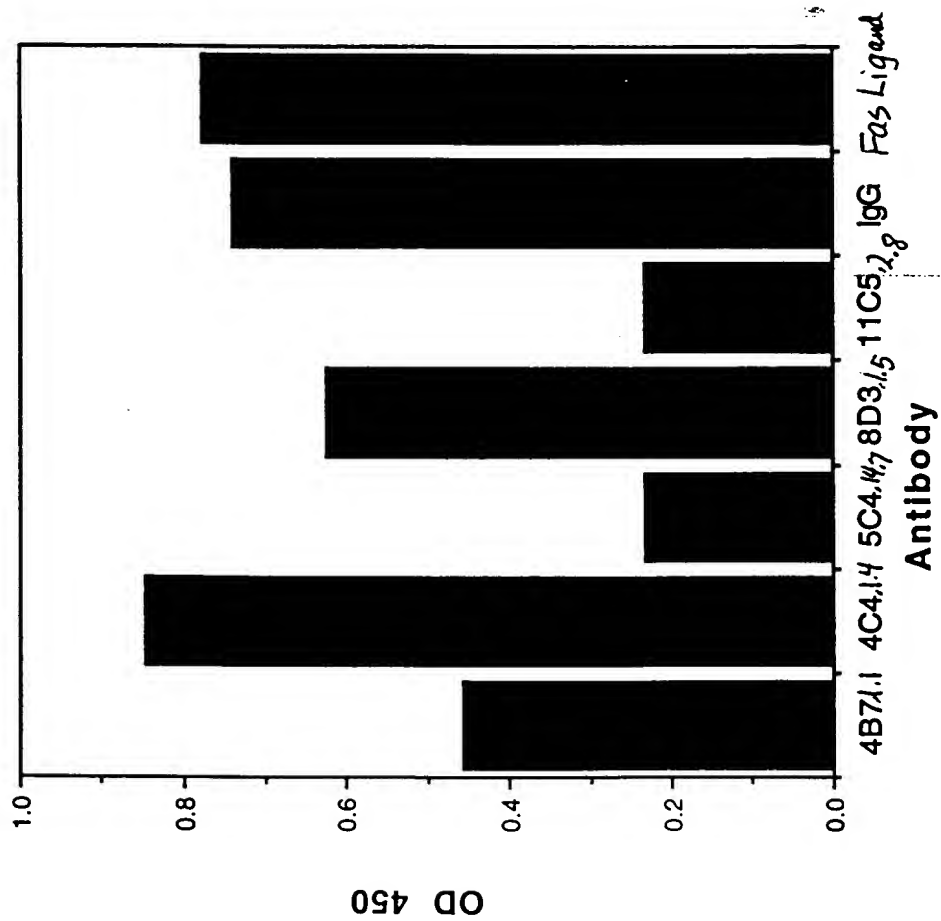


Fig. 14